
Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=12; day=2; hr=14; min=11; sec=12; ms=388;]

Reviewer Comments:

<210> 10

<211> 137

<212> PRT

<213> Artificial Sequence

The above <213> response requires explanation in the <220>-<223> section: please give the source of the genetic material. Same error in Sequences 12, 14, 16, 18, 20, and 22.

Validated By CRFValidator v 1.0.3

Application No: 10599313 Version No: 1.0

Input Set:

Output Set:

Started: 2008-10-30 15:01:37.785

Finished: 2008-10-30 15:01:40.599

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 814 ms

Total Warnings: 24

Total Errors: 7

No. of SeqIDs Defined: 35

Actual SeqID Count: 35

Err	or code	Error Description
W	213	Artificial or Unknown found in <213> in SEQ ID (1)
W	213	Artificial or Unknown found in <213> in SEQ ID (2)
W	213	Artificial or Unknown found in <213> in SEQ ID (3)
W	213	Artificial or Unknown found in <213> in SEQ ID (4)
W	213	Artificial or Unknown found in <213> in SEQ ID (9)
W	213	Artificial or Unknown found in <213> in SEQ ID (10)
E	224	$<\!220\!>\!,<\!223\!>$ section required as $<\!213\!>$ has Artificial sequence or Unknown in SEQID (10)
W	213	Artificial or Unknown found in <213> in SEQ ID (11)
W	213	Artificial or Unknown found in <213> in SEQ ID (12)
E	224	$<\!220\!>\!,<\!223\!>$ section required as $<\!213\!>$ has Artificial sequence or Unknown in SEQID (12)
W	213	Artificial or Unknown found in <213> in SEQ ID (13)
W	213	Artificial or Unknown found in <213> in SEQ ID (14)
E	224	$<\!220\!>\!,<\!223\!>$ section required as $<\!213\!>$ has Artificial sequence or Unknown in SEQID (14)
W	213	Artificial or Unknown found in <213> in SEQ ID (15)
W	213	Artificial or Unknown found in <213> in SEQ ID (16)
E	224	$<\!220\!>\!{},\!<\!223\!>$ section required as $<\!213\!>$ has Artificial sequence or Unknown in SEQID (16)
W	213	Artificial or Unknown found in <213> in SEQ ID (17)
W	213	Artificial or Unknown found in <213> in SEQ ID (18)

Input Set:

Output Set:

Started: 2008-10-30 15:01:37.785

Finished: 2008-10-30 15:01:40.599

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 814 ms

Total Warnings: 24

Total Errors: 7

No. of SeqIDs Defined: 35

Actual SeqID Count: 35

Err	or code	Error Description
E	224	<220>, $<223>$ section required as $<213>$ has Artificial sequence or Unknown in SEQID (18)
W	213	Artificial or Unknown found in <213> in SEQ ID (19)
W	213	Artificial or Unknown found in <213> in SEQ ID (20)
E	224	$<\!220\!>\!,<\!223\!>$ section required as $<\!213\!>$ has Artificial sequence or Unknown in SEQID (20)
W	213	Artificial or Unknown found in <213> in SEQ ID (21)
W	213	Artificial or Unknown found in <213> in SEQ ID (22)
E	224	$<\!220\!>\!{},<\!223\!>$ section required as $<\!213\!>$ has Artificial sequence or Unknown in SEQID (22)
W	213	Artificial or Unknown found in <213> in SEQ ID (23)
W	213	Artificial or Unknown found in $<213>$ in SEQ ID (24) This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING

<110>	POSCO	
	POSTECH Foundation	
CHA,	Hyung Joon	
NAWH	G, Dong Soo	
<120>	Mussel Bioadhesive	
<130>	20010-06USA	
	10599313	
<141>	2008-10-30	
<150×	PCT/KR2005/000888	
<150>		
\131 <i>></i>	2003 03 23	
<150>	US 60/556,805	
<151>	2004-03-26	
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<170>	KopatentIn 1.71	
<210>	1	
<211>	30	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
. 4 0 0 .	7	
<400>	1	20
ggeerg	cagc agttctgaag aatacaaggg	30
<210>	2	
<211>	29	
<212>	DNA	
<213>	Artificial Sequence	
	-	
<220>		
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<400>	2	
gtagat	ctat acgccggacc agtgaacag	29
_	_	
<210>	3	
<211>	21	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<u> </u>		

<223> primer

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                                                                           21
<210>
        4
<211>
         21
<212>
        DNA
<213>
        Artificial Sequence
<220>
<223>
        primer
<400>
         4
                                                                           21
aaaaacagcg gaaaatacaa g
<210>
<211>
        228
<212>
        DNA
<213>
       Mytilus galloprovincialis
<220>
<221>
       CDS
<222>
        (1)..(228)
<223>
       Mytilus galloprovincialis foot protein-5 cDNA
<400>
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                                                                           48
Ser Ser Glu Glu Tyr Lys Gly Gly Tyr Tyr Pro Gly Asn Thr Tyr His
 1
                                     10
                                                          15
tat cat tca ggt ggt agt tat cac gga tcc ggc tat cat gga gga tat
                                                                           96
Tyr His Ser Gly Gly Ser Tyr His Gly Ser Gly Tyr His Gly Gly Tyr
             20
                                 25
aag gga aag tat tac gga aag gca aag aaa tac tat tat aaa tat aaa
                                                                          144
Lys Gly Lys Tyr Tyr Gly Lys Ala Lys Lys Tyr Tyr Tyr Lys Tyr Lys
         35
                             40
                                                 45
                                                                          192
aac agc gga aaa tac aag tat ctg aag aaa gct aga aaa tac cat aga
Asn Ser Gly Lys Tyr Lys Tyr Leu Lys Lys Ala Arg Lys Tyr His Arg
     50
aag ggt tac aag aag tat tat gga ggt ggt agc agt
                                                                          228
Lys Gly Tyr Lys Lys Tyr Tyr Gly Gly Gly Ser Ser
 65
                     70
<210> 6
<211> 76
<212> PRT
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<213> Mytilus galloprovincialis

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Tyr His Ser Gly Gly Ser Tyr His Gly Ser Gly Tyr His Gly Gly Tyr
            2.0
                                2.5
Lys Gly Lys Tyr Tyr Gly Lys Ala Lys Lys Tyr Tyr Tyr Lys Tyr Lys
Asn Ser Gly Lys Tyr Lys Tyr Leu Lys Lys Ala Arg Lys Tyr His Arg
                        55
Lys Gly Tyr Lys Lys Tyr Tyr Gly Gly Gly Ser Ser
                    70
<210> 7
<211> 180
<212> DNA
<213> mytilus edulis
<220>
<221> CDS
<222>
       (1)..(180)
<223> 6 times repeated sequence derived from mytilus edulis foot
        protein-1
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                                                                         48
Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro
ccg act tat aag gct aaa cct agc tat cca cct acg tac aaa gct aaa
                                                                         96
Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys
            20
                                25
ccg tct tac ccg ccg act tac aaa gca aaa ccg tcc tac cct ccg acc
                                                                        144
Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr
        35
                                                                        180
tat aag gct aaa ccg agt tac ccc ccg act tac aaa
Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys
                        55
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<211> 60
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Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys

20 25 30

Pro Ser	Tyr Pro 35	Pro Thr	Tyr Lys 40	_	Pro Ser	Tyr Pro 45	Pro Thr	
Tyr Lys 50	Ala Lys	Pro Ser	Tyr Pro 55	Pro Thr	Tyr Lys			
<210> <211> <212> <213>	9 411 DNA Artific	cial Seq	uence					
<220> <223>	Bioadhe	esive pr	otein(mg	fp-150)	coding s	equence		
<220> <221> <222> <223>	CDS (1)(⁴ Bioadhe		otein(mg	fp-150)				
_	-	_	=		Ala Lys	ccc tcg Pro Ser		48
-	_	-	_		_	tac aaa Tyr Lys 30	-	96
-	=	_		Ala Lys	-	tac cct Tyr Pro 45	=	144
						agt tct Ser Ser		192
_				_		tat cat Tyr His		240
					Gly Tyr	aag gga Lys Gly		288
		_				aac agc Asn Ser 110		336
				Lys Tyr		aag ggt Lys Gly 125		384

411

aag tat tat gga ggt agc agt gaa ttc Lys Tyr Tyr Gly Gly Ser Ser Glu Phe 135 <210> 10 <211> 137 <212> PRT <213> Artificial Sequence <400> 10 Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro 5 Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys 2.5 Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr 40 Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ser Ser Glu Glu 55 Tyr Lys Gly Gly Tyr Tyr Pro Gly Asn Ser Asn His Tyr His Ser Gly 70 75 Gly Ser Tyr His Gly Ser Gly Tyr His Gly Gly Tyr Lys Gly Lys Tyr 85 Tyr Gly Lys Ala Lys Lys Tyr Tyr Lys Tyr Lys Asn Ser Gly Lys 100 105 110 Tyr Lys Tyr Leu Lys Lys Ala Arg Lys Tyr His Arg Lys Gly Tyr Lys 120 115 125 Lys Tyr Tyr Gly Gly Ser Ser Glu Phe 130 135 <210> 11 <211> 411 DNA <212>

<210> 11
<211> 411
<212> DNA
<213> Artificial Sequence

<220>
<223> Bioadhesive protein(mgfp-051) coding sequence

<220>
<221> CDS
<222> (1)..(411)
<223> Bioadhesive protein(mgfp-051)

<400> 11

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1	5	10	15

tat cat tca ggt ggt agt tat cac gga tcc ggc tac cat gga gga tat	96
Tyr His Ser Gly Gly Ser Tyr His Gly Ser Gly Tyr His Gly Gly Tyr 20 25 30	30
aag gga aag tat tac gga aag gca aag aaa tac tat tat aaa tat aaa	144
Lys Gly Lys Tyr Tyr Gly Lys Ala Lys Lys Tyr Tyr Tyr Lys Tyr Lys 35 40 45	
aac agc gga aaa tac aag tat cta aag aaa gct aga aaa tac cat aga	192
Asn Ser Gly Lys Tyr Lys Tyr Leu Lys Lys Ala Arg Lys Tyr His Arg 50 55 60	
aag ggt tac aag aag tat tat gga ggt agc agt gaa ttc gct aaa ccg	240
Lys Gly Tyr Lys Lys Tyr Tyr Gly Gly Ser Ser Glu Phe Ala Lys Pro 65 70 75 80	
tet tae eeg eeg ace tae aaa gea aaa eee teg tae eea eeg act tat	288
Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr 85 90 95	
aag gct aaa cct agc tat cca cct acg tac aaa gct aaa ccg tct tac	336
Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr 100 105 110	
ccg ccg act tac aaa gca aaa ccg tcc tac cct ccg acc tat aag gct	384
Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ala 115 120 125	
aaa ccg agt tac ccc ccg act tac aaa	411
Lys Pro Ser Tyr Pro Pro Thr Tyr Lys 130 135	
<210> 12	
<211> 137	
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<400> 12	
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Tyr His Ser Gly Gly Ser Tyr His Gly Ser Gly Tyr His Gly Gly Tyr 20 25 30	
Lys Gly Lys Tyr Tyr Gly Lys Ala Lys Lys Tyr Tyr Tyr Lys 35 40 45	
Asn Ser Gly Lys Tyr Lys Tyr Leu Lys Lys Ala Arg Lys Tyr His Arg 50 55 60	
Lys Gly Tyr Lys Lys Tyr Tyr Gly Gly Ser Ser Glu Phe Ala Lys Pro 65 70 75 80	

Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr

Lys Ala	Lys Pro	Ser Tyr	Pro Pro	Thr Tyr	Lys Ala	Lys Pro	Ser Tyr	
Pro Pro	Thr Tyr 115	Lys Ala	Lys Pro		Pro Pro	Thr Tyr	Lys Ala	
Lys Pro 130	Ser Tyr	Pro Pro	Thr Tyr	Lys				
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<220>								
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\223/	bloadile	esive bi	otein(mg	TP-131)				
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	Pro Ser		Pro Thr			Pro Ser	Tyr Pro	
1		5		10	1		15	
ccg act	tat aag	gct aaa	cct agc	tat cca	cct acq	f tac aaa	. gct aaa	96
Pro Thr	Tyr Lys	Ala Lys	Pro Ser	Tyr Pro	Pro Thi	Tyr Lys	Ala Lys	
	20			25		30		
cca tct	tac ccq	cca act	tac aaa	aca aaa	cca tca	tac cct	ccq acc	144
_		_		_	_	Tyr Pro	_	777
	35		40	_		45		
_	-			=		=	gaa gaa	192
	Ala Lys	Pro Ser	_	Pro Thi		s Ser Ser	Glu Glu	
50			55		60	l		
tac aag	ggt ggt	tat tac	cca qqc	aat tcc	aac cac	: tat cat	tca ggt	240
Tyr Lys	Gly Gly	Tyr Tyr	Pro Gly	Asn Ser	Asn His	Tyr His	Ser Gly	
65		70			75		80	
aat sat	t at	~~~ + ~~	aaa taa	ast aas			224 + 2+	200
						: aag gga : Lys Gly	=	288
1		85	1 -1	90		=1 = 0 + 1	95	
tac gga	aag gca	aag aaa	tac tat	tat aaa	ı tat aaa	aac agc	gga aaa	336
Tyr Gly	=	Lys Lys	Tyr Tyr		Tyr Lys		Gly Lys	
	100			105		110		

tac aag tat cta aag aaa gct aga aaa tac cat aga aag ggt tac aag

384

Tyr	Lys	Tyr 115	Leu	Lys	Lys	Ala	Arg 120	Lys	Tyr	His	Arg	Lys 125	Gly	Tyr	Lys		
aag Lys					_	_	_		-		_			_	_		432
acc Thr 145			-			_			_			_	-				480
agc Ser				_			_		_			_	_				528
aaa Lys .	-		-				-			_	-		_	_			576
ccc Pro	_																591
<211 <212 <213	> E	L97 PRT															
< 400	> 1	L 4			equer		Thr	Tur	Tug	או ה	Twa	Dro	Cor	Tur	Dro		
	> 1 Lys	L4 Pro	Ser Lys	Tyr 5	Pro	Pro		Tyr	10		_		Lys	15			
<400 Ala 1	>] Lys Thr	l4 Pro Tyr	Ser Lys 20	Tyr 5 Ala	Pro Lys	Pro Pro	Ser	Tyr 25	10	Pro	Thr	Tyr	Lys 30	15 Ala	Lys		
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Thr Tyr Ly 145	's Ala Ly	s Pro Ser 150	Tyr Pro	Pro Thr		Ala Lys	Pro 160
Ser Tyr Pr	o Pro Th		Ala Lys	Pro Ser	Tyr Pro	Pro Thr	Tyr
Lys Ala Ly	rs Pro Se	r Tyr Pro	Pro Thr		Ala Lys	Pro Ser 190	Tyr
Pro Pro Th		ಶ					
	.5 854						
	NA	1 0					
<213> A	rtificia	l Sequenc	e				
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	onstruct ector	for expr	ession c	f Bioadh	esive pr	otein(mg	fp-5) in pMDG05
·							
<220>							
	DS						
	1)(351)					
<223> E	Bioadhesi	ve recomb	inant pr	otein ex	pressed	in pMDG0	5 vector
	.5						
atg ggg gg	ıt tct ca						
	rt tct ca y Ser Hi						Thr
atg ggg gg Met Gly Gl 1	t tct ca y Ser Hi	s His His 5	His His	His Gly	Met Ala	Ser Met	Thr
atg ggg gg Met Gly Gl	t tct ca y Ser Hi	s His His 5 g ggt cgg	His His	His Gly 10	Met Ala	Ser Met 15 gat aag	Thr gat 96
atg ggg gg Met Gly Gl 1 ggt gga ca	t tct ca y Ser Hi	s His His 5 g ggt cgg	His His	His Gly 10 tac gac	Met Ala	Ser Met 15 gat aag	Thr gat 96
atg ggg gg Met Gly Gl 1 ggt gga ca Gly Gly Gl	nt tct ca y Ser Hi ng caa at n Gln Me 20	s His His 5 g ggt cgg t Gly Arg	His His act ctg Thr Leu 25	His Gly 10 tac gac	Met Ala gat gac Asp Asp	Ser Met 15 gat aag Asp Lys 30	Thr gat 96 Asp
atg ggg gg Met Gly Gl 1 ggt gga ca	t tct ca y Ser Hi ng caa at n Gln Me 20	s His His 5 g ggt cgg t Gly Arg	His His act ctg Thr Leu 25	His Gly 10 tac gac Tyr Asp	Met Ala gat gac Asp Asp tct gaa	Ser Met 15 gat aag Asp Lys 30 gaa tac	Thr gat 96 Asp aag 144
atg ggg gg Met Gly Gl 1 ggt gga ca Gly Gly Gl cga tgg gg Arg Trp Gl	t tct ca y Ser Hi ng caa at n Gln Me 20	s His His 5 g ggt cgg t Gly Arg	His His act ctg Thr Leu 25	His Gly 10 tac gac Tyr Asp	Met Ala gat gac Asp Asp tct gaa	Ser Met 15 gat aag Asp Lys 30 gaa tac	Thr gat 96 Asp aag 144
atg ggg gg Met Gly Gl 1 ggt gga ca Gly Gly Gl cga tgg gg Arg Trp Gl	t tct ca y Ser Hi g caa at n Gln Me 20 ga tcc ga y Ser Gl	s His His g ggt cgg t Gly Arg g ctc gag u Leu Glu	act ctg Thr Leu 25 atc tgc	His Gly 10 tac gac Tyr Asp agc agt Ser Ser	Met Ala gat gac Asp Asp tct gaa Ser Glu 45	Ser Met 15 gat aag Asp Lys 30 gaa tac Glu Tyr	Thr gat 96 Asp aag 144 Lys
atg ggg gg Met Gly Gl 1 ggt gga ca Gly Gly Gl cga tgg gg Arg Trp Gl	t tct ca y Ser Hi g caa at n Gln Me 20 ga tcc ga y Ser Gl	s His His g ggt cgg t Gly Arg g ctc gag u Leu Glu a ggc aat	act ctg Thr Leu 25 atc tgc Ile Cys 40	His Gly 10 tac gac Tyr Asp agc agt Ser Ser	Met Ala gat gac Asp Asp tct gaa Ser Glu 45 cat tca	Ser Met 15 gat aag Asp Lys 30 gaa tac Glu Tyr	Thr gat 96 Asp aag 144 Lys agt 192
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atg ggg gg Met Gly Gl 1 ggt gga ca Gly Gly Gl cga tgg gg Arg Trp Gl aggt ggt ta Gly Gly Ty 50	g caa at n Gln Me 20 ser Gl	s His His 5 g ggt cgg t Gly Arg g ctc gag u Leu Glu a ggc aat o Gly Asn 55	act ctg Thr Leu 25 atc tgc Ile Cys 40 tcg aac	His Gly 10 tac gac Tyr Asp agc agt Ser Ser cac tat His Tyr	Met Ala gat gac Asp Asp tct gaa Ser Glu 45 cat tca His Ser 60	Ser Met 15 gat aag Asp Lys 30 gaa tac Glu Tyr ggt ggt Gly Gly	gat 96 Asp aag 144 Lys agt 192 Ser
atg ggg gg Met Gly Gl 1 ggt gga ca Gly Gly Gl cga tgg gg Arg Trp Gl 3 ggt ggt ta Gly Gly Ty	t tct ca y Ser Hi g caa at n Gln Me 20 ga tcc ga y Ser Gl t tac cc r Tyr Pr	g ggt cgg t Gly Arg g ctc gag u Leu Glu a ggc aat o Gly Asn 55	act ctg Thr Leu 25 atc tgc Ile Cys 40 tcg aac Ser Asn	His Gly 10 tac gac Tyr Asp agc agt Ser Ser cac tat His Tyr	Met Ala gat gac Asp Asp tct gaa Ser Glu 45 cat tca His Ser 60 gga aag	Ser Met 15 gat aag Asp Lys 30 gaa tac Glu Tyr ggt ggt Gly Gly tat tac	gat 96 Asp 144 Lys 192 ser 240
atg ggg gg Met Gly Gl 1 ggt gga ca Gly Gly Gl cga tgg gg Arg Trp Gl 3 ggt ggt ta Gly Gly Ty 50 tat cac gg	t tct ca y Ser Hi g caa at n Gln Me 20 ga tcc ga y Ser Gl t tac cc r Tyr Pr	g ggt cgg t Gly Arg g ctc gag u Leu Glu a ggc aat o Gly Asn 55	act ctg Thr Leu 25 atc tgc Ile Cys 40 tcg aac Ser Asn	His Gly 10 tac gac Tyr Asp agc agt Ser Ser cac tat His Tyr	Met Ala gat gac Asp Asp tct gaa Ser Glu 45 cat tca His Ser 60 gga aag Gly Lys	Ser Met 15 gat aag Asp Lys 30 gaa tac Glu Tyr ggt ggt Gly Gly tat tac	gat 96 Asp 144 Lys 192 ser 240
atg ggg gg Met Gly Gl 1 ggt gga ca Gly Gly Gl cga tgg gg Arg Trp Gl 3 ggt ggt ta Gly Gly Ty 50 tat cac gg Tyr His Gl	g caa at n Gln Me 20 ser Gl	s His His 5 g ggt cgg t Gly Arg g ctc gag u Leu Glu a ggc aat o Gly Asn 55 c tac cat y Tyr His	act ctg Thr Leu 25 atc tgc Ile Cys 40 tcg aac Ser Asn gga gga	His Gly 10 tac gac Tyr Asp agc agt Ser Ser cac tat His Tyr tat aag Tyr Lys 75	Met Ala gat gac Asp Asp tct gaa Ser Glu 45 cat tca His Ser 60 gga aag Gly Lys	Ser Met 15 gat aag Asp Lys 30 gaa tac Glu Tyr ggt ggt Gly Gly tat tac Tyr Tyr	gat 96 Asp 96 aag 144 Lys 192 ser 240 Gly 80
atg ggg gg Met Gly Gl 1 ggt gga ca Gly Gly Gl cga tgg gg Arg Trp Gl 3 ggt ggt ta Gly Gly Ty 50 tat cac gg Tyr His Gl 65	g caa at an Gln Me 20 Ta tcc ga y Ser Gl Ta tcc gg Ta tcc gg Tyr Pr Ta tcc gg	g ggt cgg t Gly Arg g ctc gag u Leu Glu a ggc aat o Gly Asn 55 c tac cat y Tyr His 70 c tat tat	act ctg Thr Leu 25 atc tgc Ile Cys 40 tcg aac Ser Asn gga gga Gly Gly aaa tat	His Gly 10 tac gac Tyr Asp agc agt Ser Ser cac tat His Tyr tat aag Tyr Lys 75	Met Ala gat gac Asp Asp tct gaa Ser Glu 45 cat tca His Ser 60 gga aag Gly Lys agc gga	Ser Met 15 gat aag Asp Lys 30 gaa tac Glu Tyr ggt ggt Gly Gly tat tac Tyr Tyr aaa tac	gat 96 Asp 144 Lys 192 ser 240 Gly 80 aag 288
atg ggg gg Met Gly Gl ggt gga ca Gly Gly Gl cga tgg gg Arg Trp Gl aggt ggt ta Gly Gly Ty 50 tat cac gg Tyr His Gl 65	t tct ca y Ser Hi g caa at n Gln Me 20 ga tcc ga y Ser Gl gt tac cc r Tyr Pr ga tcc gg y Ser Gl	g ggt cgg t Gly Arg g ctc gag u Leu Glu a ggc aat o Gly Asn 55 c tac cat y Tyr His 70 c tat tat	act ctg Thr Leu 25 atc tgc Ile Cys 40 tcg aac Ser Asn gga gga Gly Gly aaa tat	His Gly 10 tac gac Tyr Asp agc agt Ser Ser cac tat His Tyr tat aag Tyr Lys 75	Met Ala gat gac Asp Asp tct gaa Ser Glu 45 cat tca His Ser 60 gga aag Gly Lys agc gga	Ser Met 15 gat aag Asp Lys 30 gaa tac Glu Tyr ggt ggt Gly Gly tat tac Tyr Tyr aaa tac	gat 96 Asp 144 Lys 192 ser 240 Gly 80 aag 288
atg ggg gg Met Gly Gl ggt gga ca Gly Gly Gl cga tgg gg Arg Trp Gl aggt ggt ta Gly Gly Ty 50 tat cac gg Tyr His Gl 65	g caa at an Gln Me 20 ser Gl ser Tyr Presser Gl ser Gl ser Gl ser Gl ser Gl ser Gl ser Tyr Presser Gl ser Tyr Presser Gl ser Tyr Presser Gl ser Tyr Presser Gl ser	g ggt cgg t Gly Arg g ctc gag u Leu Glu a ggc aat o Gly Asn 55 c tac cat y Tyr His 70 c tat tat r Tyr Tyr 5	act ctg Thr Leu 25 atc tgc Ile Cys 40 tcg aac Ser Asn gga gga Gly Gly aaa tat	His Gly 10 tac gac Tyr Asp agc agt Ser Ser cac tat His Tyr tat aag Tyr Lys 75 aaa aac Lys Asn 90	Met Ala gat gac Asp Asp tct gaa Ser Glu 45 cat tca His Ser 60 gga aag Gly Lys agc gga Ser Gly	Ser Met 15 gat aag Asp Lys 30 gaa tac Glu Tyr ggt ggt Gly Gly tat tac Tyr Tyr aaa tac Lys Tyr 95	gat 96 Asp 96 aag 144 Lys 192 ser 240 Gly 80 aag 288 Lys